

# SEQUENCE LISTING

<110> Garcia-Martinez, Leon Fernando  
Chen, Yuching  
Andrews, Dawn  
Celltech R&D, Inc.

<120> Modulating Immune Responses

<130> 1427.008US1

<160> 99

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 2051

<212> DNA

<213> Mus musculus

<400> 1

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<211> 196

<212> PRT

<213> Mus musculus

<400> 2

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Tyr	Ser	Leu	Thr	Ile	Gln	Asn	Thr	Thr	Ile	Cys	Ser	Ser	Gly	Thr	Tyr
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Ser	Ile	Phe	Pro	Asp	Ile	Ser	Lys	Pro	Gly	Thr	Glu	Gln	Ala	Phe	Leu
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Thr	Glu	Thr	Val												
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<210> 3

<211> 2051

<212> DNA

<213> Artificial Sequence

<220>

<223> A synthetic mutant CD83 sequence

<400> 3

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tcaaagaaga	atttttcatg	ttttttcaaa	gaagtgtgtt	tctttccttt	tttaaaatat	1320
gaaggtctag	ttacatagca	ttgctagctg	acaagcagcc	tgagagaaga	tggagaatgt	1380
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<210> 4  
 <211> 251  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> A synthetic mutant CD83 sequence

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<400> 4
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          20          25          30
Ala Asp Leu Pro Cys Thr Ala Pro Trp Asp Pro Gln Leu Ser Tyr Ala
          35          40          45
Val Ser Trp Ala Lys Val Ser Glu Ser Gly Thr Glu Ser Val Glu Leu
          50          55          60
Pro Glu Ser Lys Gln Asn Ser Ser Phe Glu Ala Pro Arg Arg Arg Ala
65          70          75          80
Tyr Ser Leu Thr Ile Gln Asn Thr Thr Ile Cys Ser Ser Gly Thr Tyr
          85          90          95
Arg Cys Ala Leu Gln Glu Leu Gly Gly Gln Arg Asn Leu Ser Gly Thr
          100          105          110
Val Val Leu Lys Val Thr Gly Cys Pro Lys Glu Ala Thr Glu Ser Thr
          115          120          125
Phe Arg Lys Tyr Arg Ala Glu Ala Val Leu Leu Phe Ser Leu Val Val
          130          135          140
Phe Tyr Leu Thr Leu Ile Ile Phe Thr Cys Lys Phe Ala Arg Leu Gln
145          150          155          160
Ser Ile Phe Pro Asp Ile Ser Lys Pro Gly Thr Glu Gln Ala Phe Leu
          165          170          175

Pro Val Thr Ser Pro Ser Lys His Leu Gly Pro Val Thr Leu Pro Lys
          180          185          190
Thr Glu Thr Val Arg Val Gly Ser Pro Leu Val Phe Thr Lys Pro Arg
          195          200          205
Ala His Gln Ile Ser Val Pro Glu Cys His Pro Asp Lys Arg Arg Met
          210          215          220
Ser Ser Ile Leu Arg Trp Gln Pro Phe Phe Glu Val Leu His Leu Thr
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Val Gly Ser Thr Leu Leu Pro Asp Thr Gly Ser
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<210> 5  
 <211> 756  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> A synthetic mutant CD83 sequence

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<400> 5
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tattccctga cgatccaaaa cactaccatc tgcagctcgg gcacctacag gtgtgccctg      300
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<400> 6  
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<210> 7

<211> 168

<212> DNA

<213> Artificial Sequence

<220>

<223> A synthetic mutant CD83 sequence

<400> 7

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<210> 8

<211> 55

<212> PRT

<213> Artificial Sequence

<220>

<223> A synthetic mutant CD83 sequence

<400> 8

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Arg Val Gly Ser Pro Leu Val Phe Thr Lys Pro Arg Ala His Gln Ile
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Ser Val Pro Glu Cys His Pro Asp Lys Arg Arg Met Ser Ser Ile Leu
          20          25          30
Arg Trp Gln Pro Phe Phe Glu Val Leu His Leu Thr Val Gly Ser Thr
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Leu Leu Pro Asp Thr Gly Ser
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<210> 9

<211> 205

<212> PRT

<213> Homo sapiens

<400> 9

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Ala Pro Ala Thr Pro Glu Val Lys Val Ala Cys Ser Glu Asp Val Asp
          20          25          30

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Trp	Val	Lys	Leu	Leu	Glu	Gly	Gly	Glu	Glu	Arg	Met	Glu	Thr	Pro	Gln
	50					55					60				
Glu	Asp	His	Leu	Arg	Gly	Gln	His	Tyr	His	Gln	Lys	Gly	Gln	Asn	Gly
65					70					75				80	
Ser	Phe	Asp	Ala	Pro	Asn	Glu	Arg	Pro	Tyr	Ser	Leu	Lys	Ile	Arg	Asn
			85					90						95	
Thr	Thr	Ser	Cys	Asn	Ser	Gly	Thr	Tyr	Arg	Cys	Thr	Leu	Gln	Asp	Pro
			100					105					110		
Asp	Gly	Gln	Arg	Asn	Leu	Ser	Gly	Lys	Val	Ile	Leu	Arg	Val	Thr	Gly
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Cys	Pro	Ala	Gln	Arg	Lys	Glu	Glu	Thr	Phe	Lys	Lys	Tyr	Arg	Ala	Glu
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Ile	Val	Leu	Leu	Leu	Ala	Leu	Val	Ile	Phe	Tyr	Leu	Thr	Leu	Ile	Ile
145					150					155					160
Phe	Thr	Cys	Lys	Phe	Ala	Arg	Leu	Gln	Ser	Ile	Phe	Pro	Asp	Phe	Ser
				165					170					175	
Lys	Ala	Gly	Met	Glu	Arg	Ala	Phe	Leu	Pro	Val	Thr	Ser	Pro	Asn	Lys
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<210> 10  
 <211> 2574  
 <212> DNA  
 <213> Homo sapiens

<400> 10

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<210> 11  
 <211> 239  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> A synthetic 20D04 light chain sequence

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          20           25           30
Ser Val Ser Ala Ala Val Gly Gly Thr Val Thr Ile Asn Cys Gln Ala
          35           40           45
Ser Glu Ser Ile Ser Asn Tyr Leu Ser Trp Tyr Gln Gln Lys Pro Gly
 50           55           60
Gln Pro Pro Lys Leu Leu Ile Tyr Arg Thr Ser Thr Leu Ala Ser Gly
65           70           75           80
Val Ser Ser Arg Phe Lys Gly Ser Gly Ser Gly Thr Glu Tyr Thr Leu
          85           90           95
Thr Ile Ser Gly Val Gln Cys Asp Asp Val Ala Thr Tyr Tyr Cys Gln
          100          105          110
Cys Thr Ser Gly Gly Lys Phe Ile Ser Asp Gly Ala Ala Phe Gly Gly
          115          120          125
Gly Thr Glu Val Val Val Lys Gly Asp Pro Val Ala Pro Thr Val Leu
          130          135          140
Leu Phe Pro Pro Ser Ser Asp Glu Val Ala Thr Gly Thr Val Thr Ile
145          150          155          160
Val Cys Val Ala Asn Lys Tyr Phe Pro Asp Val Thr Val Thr Trp Glu
          165          170          175
Val Asp Gly Thr Thr Gln Thr Thr Gly Ile Glu Asn Ser Lys Thr Pro
          180          185          190
Gln Asn Ser Ala Asp Cys Thr Tyr Asn Leu Ser Ser Thr Leu Thr Leu
          195          200          205
Thr Ser Thr Gln Tyr Asn Ser His Lys Glu Tyr Thr Cys Lys Val Thr
          210          215          220
Gln Gly Thr Thr Ser Val Val Gln Ser Phe Ser Arg Lys Asn Cys
225          230          235

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<210> 12  
 <211> 720  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> A synthetic 20D04 anti-CD83 light chain sequence

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<400> 12
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acagtcacca	tcaattgcc	ggccagtgaa	agcattagca	actacttata	ctggtatcag	180
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gtctcatcgc	ggttcaaagg	cagtggatct	gggacagagt	acactctcac	catcagcggc	300
gtgcagtgtg	acgatgttgc	cacttactac	tgtcaatgca	cttctggtgg	gaagttcatt	360
agtgatggg	ctgctttcgg	cggagggacc	gaggtggtgg	tcaaagggtga	tccagttgca	420
cctactgtcc	tcctcttccc	accatctagc	gatgaggtgg	caactggaac	agtcaccatc	480
gtgtgtgtgg	cgaataaata	ctttcccgat	gtcaccgtca	cctgggaggt	ggatggcacc	540
acccaaacaa	ctggcatcga	gaacagtaaa	acaccgcaga	attctgcaga	ttgtacctac	600
aacctcagca	gcactctgac	actgaccagc	acacagtaca	acagccacaa	agagtacacc	660
tgcaagggtga	cccagggcac	gacctcagtc	gtccagagct	tcagtaggaa	gaactgttaa	720

<210> 13

<211> 454

<212> PRT

<213> Artificial Sequence

<220>

<223> A synthetic 20D04 heavy chain sequence

<400> 13

Met	Glu	Thr	Gly	Leu	Arg	Trp	Leu	Leu	Leu	Val	Ala	Val	Leu	Lys	Gly
1				5					10					15	
Val	Gln	Cys	Gln	Ser	Val	Glu	Glu	Ser	Gly	Gly	Arg	Leu	Val	Thr	Pro
			20					25					30		
Gly	Thr	Pro	Leu	Thr	Leu	Thr	Cys	Thr	Val	Ser	Gly	Phe	Ser	Leu	Ser
			35				40					45			
Asn	Asn	Ala	Ile	Asn	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu
	50				55				60						
Trp	Ile	Gly	Tyr	Ile	Trp	Ser	Gly	Gly	Leu	Thr	Tyr	Tyr	Ala	Asn	Trp
65				70					75					80	
Ala	Glu	Gly	Arg	Phe	Thr	Ile	Ser	Lys	Thr	Ser	Thr	Thr	Val	Asp	Leu
				85					90					95	
Lys	Met	Thr	Ser	Pro	Thr	Ile	Glu	Asp	Thr	Ala	Thr	Tyr	Phe	Cys	Ala
			100					105					110		
Arg	Gly	Ile	Asn	Asn	Ser	Ala	Leu	Trp	Gly	Pro	Gly	Thr	Leu	Val	Thr
		115					120					125			
Val	Ser	Ser	Gly	Gln	Pro	Lys	Ala	Pro	Ser	Val	Phe	Pro	Leu	Ala	Pro
		130				135					140				
Cys	Cys	Gly	Asp	Thr	Pro	Ser	Ser	Thr	Val	Thr	Leu	Gly	Cys	Leu	Val
145				150					155					160	
Lys	Gly	Tyr	Leu	Pro	Glu	Pro	Val	Thr	Val	Thr	Trp	Asn	Ser	Gly	Thr
			165						170					175	
Leu	Thr	Asn	Gly	Val	Arg	Thr	Phe	Pro	Ser	Val	Arg	Gln	Ser	Ser	Gly
		180					185					190			
Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Ser	Val	Thr	Ser	Ser	Ser	Gln	Pro
		195				200					205				
Val	Thr	Cys	Asn	Val	Ala	His	Pro	Ala	Thr	Asn	Thr	Lys	Val	Asp	Lys
	210					215					220				
Thr	Val	Ala	Pro	Ser	Thr	Cys	Ser	Lys	Pro	Thr	Cys	Pro	Pro	Pro	Glu
225				230						235					240
Leu	Leu	Gly	Gly	Pro	Ser	Val	Phe	Ile	Phe	Pro	Pro	Lys	Pro	Lys	Asp
			245						250					255	
Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp
		260						265					270		
Val	Ser	Gln	Asp	Asp	Pro	Glu	Val	Gln	Phe	Thr	Trp	Tyr	Ile	Asn	Asn
		275					280					285			
Glu	Gln	Val	Arg	Thr	Ala	Arg	Pro	Pro	Leu	Arg	Glu	Gln	Gln	Phe	Asn
	290					295					300				
Ser	Thr	Ile	Arg	Val	Val	Ser	Thr	Leu	Pro	Ile	Ala	His	Gln	Asp	Trp
305				310						315				320	
Leu	Arg	Gly	Lys	Glu	Phe	Lys	Cys	Lys	Val	His	Asn	Lys	Ala	Leu	Pro
			325						330					335	

Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Arg Gly Gln Pro Leu Glu  
340 345 350  
Pro Lys Val Tyr Thr Met Gly Pro Pro Arg Glu Glu Leu Ser Ser Arg  
355 360 365  
Ser Val Ser Leu Thr Cys Met Ile Asn Gly Phe Tyr Pro Ser Asp Ile  
370 375 380  
Ser Val Glu Trp Glu Lys Asn Gly Lys Ala Glu Asp Asn Tyr Lys Thr  
385 390 395 400  
Thr Pro Ala Val Leu Asp Ser Asp Gly Ser Tyr Phe Leu Tyr Asn Lys  
405 410 415  
Leu Ser Val Pro Thr Ser Glu Trp Gln Arg Gly Asp Val Phe Thr Cys  
420 425 430  
Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Ile  
435 440 445  
Ser Arg Ser Pro Gly Lys  
450

<210> 14  
<211> 1362  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> A synthetic 20D04 anti-CD83 heavy chain sequence

<400> 14  
atggagacag gcttgcgctg gcttctcctg gtcgctgtgc tcaaaggtgt ccagtgtcag 60  
tcggtggagg agtccggggg tcgcctgggc acgcctggga caccctgac actcacctgc 120  
accgtctctg gattctccct cagtaacaat gcaataaact gggctccgcca ggctccaggg 180  
aaggggctag agtggatcgg atacatttgg agtgggtgggc ttacatacta cgcgaactgg 240  
gcggaaggcc gattcaccat ctccaaaacc tcgactacgg tggatctgaa gatgaccagt 300  
ccgacaatcg aggacacggc cacctatttc tgtgccagag ggattaataa ctccgctttg 360  
tggggcccag gcaccctggg caccgtctcc tcagggcaac ctaaggctcc atcagtcttc 420  
ccactggccc cctgctgctg ggacacaccc tctagcacgg tgacctggg ctgcctgggc 480  
aaaggctacc tcccggagcc agtgaccgtg acctggaact cgggcaccct caccaatggg 540  
gtacgcacct tcccgtccgt ccggcagtc tccaggtctt actcgtgag cagcgtgggtg 600  
agcgtgacct caagcagcca gcccgctcacc tgcaacgtgg cccaccagc caccaacacc 660  
aaagtggaca agaccgttgc gccctcgaca tgcagcaagc ccacgtgcc accccctgaa 720  
ctcctggggg gaccgtctgt cttcatcttc ccccaaaac ccaaggacac cctcatgatc 780  
tcacgcaccc ccgaggtcac atgcgtgggt gtggacgtga gccaggatga ccccgagggtg 840  
cagttcacat ggtacataaa caacgagcag gtgcgcaccg cccggccgccc gctacgggag 900  
cagcagttca acagcacgat ccgcgtgggt agcaccctcc ccacgcgca ccaggactgg 960  
ctgaggggca aggagttcaa gtgcaaagtc cacaacaagg cactcccggc ccccatcgag 1020  
aaaaccatct ccaaagccag agggcagccc ctggagccga aggtctacac catgggcccct 1080  
ccccgggagg agctgagcag caggtcgggt agcctgacct gcatgatcaa cggcttctac 1140  
ccttcgcaca tctcgggtga gtgggagaag aacgggaagg cagaggacaa ctacaagacc 1200  
acgccggccg tgctggacag cgacggctcc tacttctctg acaacaagct ctcagtgcac 1260  
acgagtgaat ggcagcgggg cgacgtcttc acctgctcgg tgatgcacga ggccttgac 1320  
aaccactaca cgcagaagtc catctccgcg tctccgggta aa 1362

<210> 15  
<211> 238  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> A synthetic 11G05 light chain sequence

<400> 15  
Met Asp Thr Arg Ala Pro Thr Gln Leu Leu Gly Leu Leu Leu Leu Trp  
1 5 10 15



Leu	Pro	Gly	Ala	Arg	Cys	Ala	Asp	Val	Val	Met	Thr	Gln	Thr	Pro	Ala
			20					25					30		
Ser	Val	Ser	Ala	Ala	Val	Gly	Gly	Thr	Val	Thr	Ile	Asn	Cys	Gln	Ser
		35					40					45			
Ser	Lys	Asn	Val	Tyr	Asn	Asn	Asn	Trp	Leu	Ser	Trp	Phe	Gln	Gln	Lys
	50					55					60				
Pro	Gly	Gln	Pro	Pro	Lys	Leu	Leu	Ile	Tyr	Tyr	Ala	Ser	Thr	Leu	Ala
65					70				75					80	
Ser	Gly	Val	Pro	Ser	Arg	Phe	Arg	Gly	Ser	Gly	Ser	Gly	Thr	Gln	Phe
			85					90					95		
Thr	Leu	Thr	Ile	Ser	Asp	Val	Gln	Cys	Asp	Asp	Ala	Ala	Thr	Tyr	Tyr
			100					105					110		
Cys	Ala	Gly	Asp	Tyr	Ser	Ser	Ser	Ser	Asp	Asn	Gly	Phe	Gly	Gly	Gly
		115					120					125			
Thr	Glu	Val	Val	Val	Lys	Gly	Asp	Pro	Val	Ala	Pro	Thr	Val	Leu	Leu
	130					135					140				
Phe	Pro	Pro	Ser	Ser	Asp	Glu	Val	Ala	Thr	Gly	Thr	Val	Thr	Ile	Val
145					150					155				160	
Cys	Val	Ala	Asn	Lys	Tyr	Phe	Pro	Asp	Val	Thr	Val	Thr	Trp	Glu	Val
			165					170					175		
Asp	Gly	Thr	Thr	Gln	Thr	Thr	Gly	Ile	Glu	Asn	Ser	Lys	Thr	Pro	Gln
			180					185					190		
Asn	Ser	Ala	Asp	Cys	Thr	Tyr	Asn	Leu	Ser	Ser	Thr	Leu	Thr	Leu	Thr
		195					200					205			
Ser	Thr	Gln	Tyr	Asn	Ser	His	Lys	Glu	Tyr	Thr	Cys	Lys	Val	Thr	Gln
	210					215					220				
Gly	Thr	Thr	Ser	Val	Val	Gln	Ser	Phe	Ser	Arg	Lys	Asn	Cys		
225					230					235					

<210> 16

<211> 717

<212> DNA

<213> Artificial Sequence

<220>

<223> A synthetic 11G05 anti-CD83 light chain sequence

<400> 16

atggacacca	gggccccac	tcagctgctg	gggctcctgc	tgctctggct	cccaggtgcc	60
agatgtgccg	acgtcgtgat	gaccagact	ccagcctccg	tgtctgcagc	tgtgggaggc	120
acagtcacca	tcaattgcc	gtccagtaag	aatgtttata	ataacaactg	gttatcctgg	180
tttcagcaga	aaccaggga	gcctccaag	ctcctgatct	attatgcac	cactctggca	240
tctgggggtcc	catcgcggt	cagaggcagt	ggatctggga	cacagttcac	tctcaccatt	300
agcgacgtgc	agtgtgacga	tgctgccact	tactactgtg	caggcgatta	tagtagtagt	360
agtgataatg	gtttcggcgg	agggaccgag	gtggtgggtca	aaggtgatcc	agttgcacct	420
actgtcctcc	tcttcccacc	atctagcgat	gaggtggcaa	ctggaacagt	caccatcgtg	480
tgtgtggcga	ataaatactt	tcccgatgtc	accgtcacct	gggaggtgga	tggcaccacc	540
caaacaactg	gcacgcagaa	cagtaaaaca	ccgcagaatt	ctgcagattg	tacctacaac	600
ctcagcagca	ctctgacact	gaccagcaca	cagtacaaca	gccacaaaga	gtacacctgc	660
aaggtgaccc	agggcacgac	ctcagtcgtc	cagagcttca	gtaggaagaa	ctgttaa	717

<210> 17

<211> 452

<212> PRT

<213> Artificial Sequence

<220>

<223> A synthetic 11G05 heavy chain sequence

<400> 17

Met	Glu	Thr	Gly	Leu	Arg	Trp	Leu	Leu	Leu	Val	Ala	Val	Leu	Lys	Gly
1				5					10					15	

Val	Gln	Cys	Gln	Ser	Val	Glu	Glu	Ser	Gly	Gly	Arg	Leu	Val	Thr	Pro
			20					25					30		
Gly	Thr	Pro	Leu	Thr	Leu	Thr	Cys	Thr	Val	Ser	Gly	Phe	Thr	Ile	Ser
		35					40					45			
Asp	Tyr	Asp	Leu	Ser	Trp	Val	Arg	Gln	Ala	Pro	Gly	Glu	Gly	Leu	Lys
	50					55					60				
Tyr	Ile	Gly	Phe	Ile	Ala	Ile	Asp	Gly	Asn	Pro	Tyr	Tyr	Ala	Thr	Trp
65					70					75					80
Ala	Lys	Gly	Arg	Phe	Thr	Ile	Ser	Lys	Thr	Ser	Thr	Thr	Val	Asp	Leu
				85					90					95	
Lys	Ile	Thr	Ala	Pro	Thr	Thr	Glu	Asp	Thr	Ala	Thr	Tyr	Phe	Cys	Ala
			100					105						110	
Arg	Gly	Ala	Gly	Asp	Leu	Trp	Gly	Pro	Gly	Thr	Leu	Val	Thr	Val	Ser
		115					120					125			
Ser	Gly	Gln	Pro	Lys	Ala	Pro	Ser	Val	Phe	Pro	Leu	Ala	Pro	Cys	Cys
	130					135					140				
Gly	Asp	Thr	Pro	Ser	Ser	Thr	Val	Thr	Leu	Gly	Cys	Leu	Val	Lys	Gly
145					150					155					160
Tyr	Leu	Pro	Glu	Pro	Val	Thr	Val	Thr	Trp	Asn	Ser	Gly	Thr	Leu	Thr
				165					170					175	
Asn	Gly	Val	Arg	Thr	Phe	Pro	Ser	Val	Arg	Gln	Ser	Ser	Gly	Leu	Tyr
			180					185					190		
Ser	Leu	Ser	Ser	Val	Val	Ser	Val	Thr	Ser	Ser	Ser	Gln	Pro	Val	Thr
		195					200					205			
Cys	Asn	Val	Ala	His	Pro	Ala	Thr	Asn	Thr	Lys	Val	Asp	Lys	Thr	Val
	210					215					220				
Ala	Pro	Ser	Thr	Cys	Ser	Lys	Pro	Thr	Cys	Pro	Pro	Pro	Glu	Leu	Leu
225					230					235					240
Gly	Gly	Pro	Ser	Val	Phe	Ile	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu
				245					250					255	
Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser
			260					265					270		
Gln	Asp	Asp	Pro	Glu	Val	Gln	Phe	Thr	Trp	Tyr	Ile	Asn	Asn	Glu	Gln
			275				280					285			
Val	Arg	Thr	Ala	Arg	Pro	Pro	Leu	Arg	Glu	Gln	Gln	Phe	Asn	Ser	Thr
	290					295					300				
Ile	Arg	Val	Val	Ser	Thr	Leu	Pro	Ile	Ala	His	Gln	Asp	Trp	Leu	Arg
305					310					315					320
Gly	Lys	Glu	Phe	Lys	Cys	Lys	Val	His	Asn	Lys	Ala	Leu	Pro	Ala	Pro
				325					330					335	
Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	Arg	Gly	Gln	Pro	Leu	Glu	Pro	Lys
			340					345					350		
Val	Tyr	Thr	Met	Gly	Pro	Pro	Arg	Glu	Glu	Leu	Ser	Ser	Arg	Ser	Val
		355					360					365			
Ser	Leu	Thr	Cys	Met	Ile	Asn	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ser	Val
	370					375					380				
Glu	Trp	Glu	Lys	Asn	Gly	Lys	Ala	Glu	Asp	Asn	Tyr	Lys	Thr	Thr	Pro
385					390					395					400
Ala	Val	Leu	Asp	Ser	Asp	Gly	Ser	Tyr	Phe	Leu	Tyr	Asn	Lys	Leu	Ser
				405					410					415	
Val	Pro	Thr	Ser	Glu	Trp	Gln	Arg	Gly	Asp	Val	Phe	Thr	Cys	Ser	Val
			420					425					430		
Met	His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr	Gln	Lys	Ser	Ile	Ser	Arg
		435				440						445			
Ser	Pro	Gly	Lys												
			450												

<210> 18  
 <211> 1356  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> A synthetic 11G05 anti-CD83 heavy chain sequence

<400> 18

atggagacag	gcctgcgctg	gcttctcctg	gtcgtgtg	tcaaaggtgt	ccagtgtcag	60
tcgggtggagg	agtccggggg	tcgcctggtc	acgcctggga	cacccttgac	actcacctgc	120
acagtctctg	gattcaccat	cagtgactac	gacttgagct	gggtccgcca	ggctccaggg	180
gaggggctga	aatacatcgg	attcattgct	attgatggta	accatacta	cgcgacctgg	240
gcaaaaggcc	gattcaccat	ctccaaaacc	tcgaccacgg	tggatctgaa	aatcaccgct	300
ccgacaaccg	aagacacggc	cacgtatttc	tgtgccagag	gggcagggga	cctctggggc	360
ccagggaccc	tcgtcaccgt	ctcttcaggg	caacctaaag	ctccatcagt	cttcccactg	420
gccccctgct	gcggggacac	accctctagc	acggtgacct	tgggctgcct	ggtcaaaggc	480
tacctcccg	agccagtgac	cgtgacctgg	aactcgggca	ccctcaccaa	tggggtacgc	540
accttcccgt	ccgtccggca	gtcctcaggc	ctctactcgc	tgagcagcgt	ggtgagcgtg	600
acctcaagca	gccagcccgt	cacctgcaac	gtggcccacc	cagccacca	caccaaagtg	660
gacaagaccg	ttgcgccctc	gacatgcagc	aagcccacgt	gcccaccccc	tgaactcctg	720
gggggaccgt	ctgtcttcat	cttcccccca	aaacccaagg	acaccctcat	gatctcacgc	780
acccccgagg	tcacatgcgt	ggtggtggac	gtgagccagg	atgacccccga	ggtgcagttc	840
acatggtaca	taaacaacga	gcagggtgcg	accgcccggc	cgccgctacg	ggagcagcag	900
ttcaacagca	cgatccgcgt	ggtcagcacc	ctccccatcg	cgcaccagga	ctggctgagg	960
ggcaaggagt	tcaagtgcaa	agtccacaac	aaggcactcc	cggcccccat	cgagaaaacc	1020
atctccaaag	ccagagggca	gccccctggg	ccgaaggctc	acaccatggg	ccctccccgg	1080
gaggagctga	gcagcaggtc	ggtcagcctg	acctgcatga	tcaacggctt	ctacccttcc	1140
gacatctcgg	tggagtggga	gaagaacggg	aaggcagagg	acaactacaa	gaccacgccg	1200
gccgtgctgg	acagcgacgg	ctcctacttc	ctctacaaca	agctctcagt	gcccacgagt	1260
gagtggcagc	ggggcgacgt	cttcacctgc	tccgtgatgc	acgaggcctt	gcacaaccac	1320
tacacgcaga	agtccatctc	ccgctctccg	ggtaaa			1356

<210> 19

<211> 238

<212> PRT

<213> Artificial Sequence

<220>

<221> SITE

<222> (1)...(238)

<223> Xaa = any amino acid

<220>

<223> A synthetic 14C12 light chain sequence

<400> 19

Met	Asp	Xaa	Arg	Ala	Pro	Thr	Gln	Leu	Leu	Gly	Leu	Leu	Leu	Leu	Trp
1				5				10						15	
Leu	Pro	Gly	Ala	Arg	Cys	Ala	Leu	Val	Met	Thr	Gln	Thr	Pro	Ala	Ser
			20					25					30		
Val	Ser	Ala	Ala	Val	Gly	Gly	Thr	Val	Thr	Ile	Asn	Cys	Gln	Ser	Ser
		35					40					45			
Gln	Ser	Val	Tyr	Asp	Asn	Asp	Glu	Leu	Ser	Trp	Tyr	Gln	Gln	Lys	Pro
		50				55					60				
Gly	Gln	Pro	Pro	Lys	Leu	Leu	Ile	Tyr	Leu	Ala	Ser	Lys	Leu	Ala	Ser
65					70					75				80	
Gly	Val	Pro	Ser	Arg	Phe	Lys	Gly	Ser	Gly	Ser	Gly	Thr	Gln	Phe	Ala
				85				90						95	
Leu	Thr	Ile	Ser	Gly	Val	Gln	Cys	Asp	Asp	Ala	Ala	Thr	Tyr	Tyr	Cys
			100					105					110		
Gln	Ala	Thr	His	Tyr	Ser	Ser	Asp	Trp	Tyr	Leu	Thr	Phe	Gly	Gly	Gly
		115					120					125			
Thr	Glu	Val	Val	Val	Lys	Gly	Asp	Pro	Val	Ala	Pro	Thr	Val	Leu	Leu
	130					135					140				
Phe	Pro	Pro	Ser	Ser	Asp	Glu	Val	Ala	Thr	Gly	Thr	Val	Thr	Ile	Val
145					150					155					160



Lys	Gly	Tyr	Leu	Pro	Glu	Pro	Val	Thr	Val	Thr	Trp	Asn	Ser	Gly	Thr
				165					170					175	
Leu	Thr	Asn	Gly	Val	Arg	Thr	Phe	Pro	Ser	Val	Arg	Gln	Ser	Ser	Gly
			180					185					190		
Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Ser	Val	Thr	Ser	Ser	Ser	Gln	Pro
		195					200					205			
Val	Thr	Cys	Asn	Val	Ala	His	Pro	Ala	Thr	Asn	Thr	Lys	Val	Asp	Lys
	210					215				220					
Thr	Val	Ala	Pro	Ser	Thr	Cys	Ser	Lys	Pro	Thr	Cys	Pro	Pro	Pro	Glu
225					230					235					240
Leu	Leu	Gly	Gly	Pro	Ser	Val	Phe	Ile	Phe	Pro	Pro	Lys	Pro	Lys	Asp
				245					250					255	
Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp
			260					265					270		
Val	Ser	Gln	Asp	Asp	Pro	Glu	Val	Gln	Phe	Thr	Trp	Tyr	Ile	Asn	Asn
	275						280					285			
Glu	Gln	Val	Arg	Thr	Ala	Arg	Pro	Pro	Leu	Arg	Glu	Gln	Gln	Phe	Asn
	290					295				300					
Ser	Thr	Ile	Arg	Val	Val	Ser	Thr	Leu	Pro	Ile	Ala	His	Gln	Asp	Trp
305					310				315						320
Leu	Arg	Gly	Lys	Glu	Phe	Lys	Cys	Lys	Val	His	Asn	Lys	Ala	Leu	Pro
				325					330					335	
Ala	Pro	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	Arg	Gly	Gln	Pro	Leu	Glu
			340					345					350		
Pro	Lys	Val	Tyr	Thr	Met	Gly	Pro	Pro	Arg	Glu	Glu	Leu	Ser	Ser	Arg
	355						360					365			
Ser	Val	Ser	Leu	Thr	Cys	Met	Ile	Asn	Gly	Phe	Tyr	Pro	Ser	Asp	Ile
	370					375				380					
Ser	Val	Glu	Trp	Glu	Lys	Asn	Gly	Lys	Ala	Glu	Asp	Asn	Tyr	Lys	Thr
385					390					395					400
Thr	Pro	Ala	Val	Leu	Asp	Ser	Asp	Gly	Ser	Tyr	Phe	Leu	Tyr	Asn	Lys
				405				410						415	
Leu	Ser	Val	Pro	Thr	Ser	Glu	Trp	Gln	Arg	Gly	Asp	Val	Phe	Thr	Cys
			420					425					430		
Ser	Val	Met	His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr	Gln	Lys	Ser	Ile
	435						440					445			
Ser	Arg	Ser	Pro	Gly	Lys										
	450														

<210> 22

<211> 1362

<212> PRT

<213> Artificial Sequence

<220>

<223> A synthetic 14C12 anti-CD83 heavy chain sequence

<400> 22

Ala	Thr	Gly	Gly	Ala	Gly	Ala	Cys	Ala	Gly	Gly	Cys	Cys	Thr	Gly	Cys
1				5					10					15	
Gly	Cys	Thr	Gly	Gly	Cys	Thr	Thr	Cys	Thr	Cys	Cys	Thr	Gly	Gly	Thr
			20					25					30		
Cys	Gly	Cys	Thr	Gly	Thr	Gly	Cys	Thr	Cys	Ala	Ala	Ala	Gly	Gly	Thr
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Gly	Gly	Ala	Gly	Cys	Thr	Gly	Ala	Gly	Cys	Ala	Gly	Cys	Ala	Gly	Gly			
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 Cys Thr Ala Cys Cys Cys Thr Thr Cys Cys Gly Ala Cys Ala Thr Cys  
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 Thr Cys Gly Gly Thr Gly Gly Ala Gly Thr Gly Gly Gly Ala Gly Ala  
 1155 1160 1165  
 Ala Gly Ala Ala Cys Gly Gly Gly Ala Ala Gly Gly Cys Ala Gly Ala  
 1170 1175 1180  
 Gly Gly Ala Cys Ala Cys Thr Ala Cys Ala Ala Gly Ala Cys Cys  
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 Ala Cys Ala Gly Cys Gly Ala Cys Gly Gly Cys Thr Cys Cys Thr Ala  
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 Cys Thr Thr Cys Cys Thr Cys Thr Ala Cys Ala Ala Cys Ala Ala Gly  
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1 5 10 15  
Val Gln Cys Gln Ser Val Glu Glu Ser Gly Gly Arg Leu Val Thr Pro  
20 25 30  
Gly Thr Pro Leu Thr Leu Thr Cys Thr Val Ser Gly Phe Ser Leu Ser  
35 40 45  
Ser Tyr Asp Met Thr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu  
50 55 60  
Trp Ile Gly Ile Ile Tyr Ala Ser Gly Ser Thr Tyr Tyr Ala Ser Trp  
65 70 75 80  
Ala Lys Gly Arg Phe Thr Ile Ser Lys Thr Ser Thr Thr Val Asp Leu  
85 90 95  
Glu Val Thr Ser Leu Thr Thr Glu Asp Thr Ala Thr Tyr Phe Cys Ser  
100 105 110  
Arg Glu His Ala Gly Tyr Ser Gly Asp Thr Gly His Leu Trp Gly Pro  
115 120 125  
Gly Thr Leu Val Thr Val Ser Ser Gly Gln Pro Lys Ala Pro Ser Val  
130 135 140  
Phe Pro Leu Ala Pro Cys Cys Gly Asp Thr Pro Ser Ser  
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<400> 53  
Met Glu Thr Gly Leu Arg Trp Leu Leu Leu Val Ala Val Leu Lys Gly  
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Val Gln Cys Gln Ser Val Glu Glu Ser Gly Gly Arg Leu Val Ser Pro  
20 25 30  
Gly Thr Pro Leu Thr Leu Thr Cys Thr Ala Ser Gly Phe Ser Leu Ser  
35 40 45  
Ser Tyr Asp Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu  
50 55 60  
Tyr Ile Gly Ile Ile Ser Ser Ser Gly Thr Thr Tyr Tyr Ala Asn Trp  
65 70 75 80  
Ala Lys Gly Arg Phe Thr Ile Ser Lys Thr Ser Thr Thr Val Asp Leu  
85 90 95  
Lys Val Thr Ser Pro Thr Ile Gly Asp Thr Ala Thr Tyr Phe Cys Ala  
100 105 110  
Arg Glu Gly Ala Gly Val Ser Met Thr Leu Trp Gly Pro Gly Thr Leu  
115 120 125  
Val Thr Val Ser Ser Gly Gln Pro Lys Ala Pro Ser Val Phe Pro Leu  
130 135 140  
Ala Pro Cys Cys Gly Asp Thr Pro Ser Ser  
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<400> 54  
Met Glu Thr Gly Leu Arg Trp Leu Leu Leu Val Ala Val Leu Lys Gly  
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Val Gln Cys Gln Ser Val Glu Glu Ser Gly Gly Arg Leu Val Thr Pro  
20 25 30  
Gly Thr Pro Leu Thr Leu Thr Cys Thr Val Ser Gly Phe Ser Leu Ser  
35 40 45  
Ser Tyr Asp Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu  
50 55 60  
Trp Ile Gly Ile Ile Tyr Ala Ser Gly Ser Thr Tyr Tyr Ala Ser Trp  
65 70 75 80  
Ala Lys Gly Arg Val Ala Ile Ser Lys Thr Ser Thr Thr Val Asp Leu  
85 90 95  
Lys Ile Thr Ser Pro Thr Thr Glu Asp Thr Ala Thr Tyr Phe Cys Ala  
100 105 110  
Arg Glu Asp Ala Gly Phe Ser Asn Ala Leu Trp Gly Pro Gly Thr Leu  
115 120 125  
Val Thr Val Ser Ser Gly Gln Pro Lys Ala Pro Ser Val Phe Pro Leu  
130 135 140  
Ala Pro Cys Cys Gly Asp Thr Pro Ser Ser  
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Met Asp Met Arg Ala Pro Thr Gln Leu Leu Gly Leu Leu Leu Leu Trp  
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Leu Pro Gly Ala Arg Cys Ala Tyr Asp Met Thr Gln Thr Pro Ala Ser  
20 25 30  
Val Glu Val Ala Val Gly Gly Thr Val Thr Ile Lys Cys Gln Ala Ser  
35 40 45  
Gln Ser Ile Ser Thr Tyr Leu Asp Trp Tyr Gln Gln Lys Pro Gly Gln  
50 55 60  
Pro Pro Lys Leu Leu Ile Tyr Asp Ala Ser Asp Leu Ala Ser Gly Val  
65 70 75 80  
Pro Ser Arg Phe Lys Gly Ser Gly Ser Gly Thr Gln Phe Thr Leu Thr  
85 90 95  
Ile Ser Asp Leu Glu Cys Ala Asp Ala Ala Thr Tyr Tyr Cys Gln Gln  
100 105 110  
Gly Tyr Thr His Ser Asn Val Asp Asn Val Phe Gly Gly Gly Thr Glu  
115 120 125  
Val Val Val Lys Gly Asp Pro Val Ala Pro Thr Val Leu Leu Phe Pro  
130 135 140  
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<210> 56  
<211> 147  
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Leu Pro Gly Ala Arg Cys Ala Tyr Asp Met Thr Gln Thr Pro Ala Ser  
20 25 30  
Val Glu Val Ala Val Gly Gly Thr Val Ala Ile Lys Cys Gln Ala Ser  
35 40 45  
Gln Ser Val Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln  
50 55 60  
Pro Pro Lys Pro Leu Ile Tyr Glu Ala Ser Met Leu Ala Ala Gly Val  
65 70 75 80  
Ser Ser Arg Phe Lys Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr  
85 90 95  
Ile Ser Asp Leu Glu Cys Asp Asp Ala Ala Thr Tyr Tyr Cys Gln Gln  
100 105 110  
Gly Tyr Ser Ile Ser Asp Ile Asp Asn Ala Phe Gly Gly Gly Thr Glu  
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Val Val Val Lys Gly Asp Pro Val Ala Pro Thr Val Leu Leu Phe Pro  
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Pro Ser Ser  
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<210> 57  
<211> 150  
<212> PRT  
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<220>  
<223> A synthetic anti-CD83 light chain variable region  
sequence

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Met Asp Met Arg Ala Pro Thr Gln Leu Leu Gly Leu Leu Leu Leu Trp  
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Leu Pro Gly Ala Arg Cys Ala Asp Val Val Met Thr Gln Thr Pro Ala  
20 25 30  
Ser Val Ser Ala Ala Val Gly Gly Thr Val Thr Ile Asn Cys Gln Ala  
35 40 45  
Ser Glu Ser Ile Ser Asn Tyr Leu Ser Trp Tyr Gln Gln Lys Pro Gly  
50 55 60  
Gln Pro Pro Lys Leu Leu Ile Tyr Arg Thr Ser Thr Leu Ala Ser Gly  
65 70 75 80  
Val Ser Ser Arg Phe Lys Gly Ser Gly Ser Gly Thr Glu Tyr Thr Leu  
85 90 95  
Thr Ile Ser Gly Val Gln Cys Asp Asp Val Ala Thr Tyr Tyr Cys Gln  
100 105 110  
Cys Thr Ser Gly Gly Lys Phe Ile Ser Asp Gly Ala Ala Phe Gly Gly  
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Gly Thr Glu Val Val Val Lys Gly Asp Pro Val Ala Pro Thr Val Leu  
130 135 140  
Leu Phe Pro Pro Ser Ser  
145 150

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<220>  
<223> A synthetic M83 020B08L light chain sequence

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Leu Pro Gly Ala Arg Cys Ala Tyr Asp Met Thr Gln Thr Pro Ala Ser  
20 25 30  
Val Glu Val Ala Val Gly Gly Thr Val Thr Ile Lys Cys Gln Ala Ser  
35 40 45  
Gln Ser Ile Ser Thr Tyr Leu Asp Trp Tyr Gln Gln Lys Pro Gly Gln  
50 55 60  
Pro Pro Lys Leu Leu Ile Tyr Asp Ala Ser Asp Leu Ala Ser Gly Val  
65 70 75 80  
Pro Ser Arg Phe Lys Gly Ser Gly Ser Gly Thr Gln Phe Thr Leu Thr  
85 90 95  
Ile Ser Asp Leu Glu Cys Ala Asp Ala Ala Thr Tyr Tyr Cys Gln Gln  
100 105 110  
Gly Tyr Thr His Ser Asn Val Asp Asn Val Phe Gly Gly Gly Thr Glu  
115 120 125  
Val Val Val Lys Gly Asp Pro Val Ala Pro Thr Val Leu Leu Phe Pro  
130 135 140  
Pro Ser Ser Asp Glu Val Ala Thr Gly Thr Val Thr Ile Val Cys Val  
145 150 155 160  
Ala Asn Lys Tyr Phe Pro Asp Val Thr Val Thr Trp Glu Val Asp Gly  
165 170 175  
Thr Thr Gln Thr Thr Gly Ile Glu Asn Ser Lys Thr Pro Gln Asn Ser  
180 185 190  
Ala Asp Cys Thr Tyr Asn Leu Ser Ser Thr Leu Thr Leu Thr Ser Thr  
195 200 205  
Gln Tyr Asn Ser His Lys Glu Tyr Thr Cys Lys Val Thr Gln Gly Thr  
210 215 220  
Thr Ser Val Val Gln Ser Phe Ser Arg Lys Asn Cys  
225 230 235

<210> 59  
<211> 711  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> A synthetic M83 020B08L anti-CD83 light chain sequence

<400> 59  
atggacatga gggccccac tcagctgctg gggctcctgc tgctctggct cccaggtgcc 60  
agatgtgcct atgatatgac ccagactcca gcctctgtgg aggtagctgt gggaggcaca 120  
gtcaccatca agtgccaggc cagtcagagc attagtagctg gtagtagctg gtatcagcag 180  
aaaccagggc agcctcccaa gctcctgata tatgatgcat ccgatctggc atctgggggtc 240  
ccatcgcggt tcaaaggcag tggatctggg acacagttca ctctcaccat cagcgacctg 300  
gagtgtgccg atgctgccac ttactactgt caacagggtt atacacatag taatgttgat 360  
aatgttttcg gcggagggac cgaggtgggt gtcaaagggt atccagttgc acctactgtc 420  
ctcctcttcc caccatctag cgatgagggt gcaactggaa cagtcaccat cgtgtgtgtg 480  
gcgaataaat actttcccga tgtcaccgtc acctgggagg tggatggcac caccctcaga 540  
actggcatcg agaacagtaa aacaccgcag aattctgcag attgtaccta caacctcagc 600  
agcactctga cactgaccag cacacagtac aacagccaca aagagtacac ctgcaagggtg 660  
accaggggca cgacctcagt cgtccagagc ttcagtagga agaactgtta a 711

<210> 60  
<211> 456  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> A synthetic M83 020B08H heavy chain sequence



<400> 60

Met	Glu	Thr	Gly	Leu	Arg	Trp	Leu	Leu	Leu	Val	Ala	Val	Leu	Lys	Gly	1	5	10	15
Val	Gln	Cys	Gln	Ser	Val	Glu	Glu	Ser	Gly	Gly	Arg	Leu	Val	Thr	Pro	20	25	30	
Gly	Thr	Pro	Leu	Thr	Leu	Thr	Cys	Thr	Val	Ser	Gly	Phe	Ser	Leu	Ser	35	40	45	
Ser	Tyr	Asp	Met	Thr	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	50	55	60	
Trp	Ile	Gly	Ile	Ile	Tyr	Ala	Ser	Gly	Thr	Thr	Tyr	Tyr	Ala	Asn	Trp	65	70	75	80
Ala	Lys	Gly	Arg	Phe	Thr	Ile	Ser	Lys	Thr	Ser	Thr	Thr	Val	Asp	Leu	85	90	95	
Lys	Val	Thr	Ser	Pro	Thr	Ile	Gly	Asp	Thr	Ala	Thr	Tyr	Phe	Cys	Ala	100	105	110	
Arg	Glu	Gly	Ala	Gly	Val	Ser	Met	Thr	Leu	Trp	Gly	Pro	Gly	Thr	Leu	115	120	125	
Val	Thr	Val	Ser	Ser	Gly	Gln	Pro	Lys	Ala	Pro	Ser	Val	Phe	Pro	Leu	130	135	140	
Ala	Pro	Cys	Cys	Gly	Asp	Thr	Pro	Ser	Ser	Thr	Val	Thr	Leu	Gly	Cys	145	150	155	160
Leu	Val	Lys	Gly	Tyr	Leu	Pro	Glu	Pro	Val	Thr	Val	Thr	Trp	Asn	Ser	165	170	175	
Gly	Thr	Leu	Thr	Asn	Gly	Val	Arg	Thr	Phe	Pro	Ser	Val	Arg	Gln	Ser	180	185	190	
Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Ser	Val	Thr	Ser	Ser	Ser	195	200	205	
Gln	Pro	Val	Thr	Cys	Asn	Val	Ala	His	Pro	Ala	Thr	Asn	Thr	Lys	Val	210	215	220	
Asp	Lys	Thr	Val	Ala	Pro	Ser	Thr	Cys	Ser	Lys	Pro	Thr	Cys	Pro	Pro	225	230	235	240
Pro	Glu	Leu	Leu	Gly	Gly	Pro	Ser	Val	Phe	Ile	Phe	Pro	Pro	Lys	Pro	245	250	255	
Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	260	265	270	
Val	Asp	Val	Ser	Gln	Asp	Asp	Pro	Glu	Val	Gln	Phe	Thr	Trp	Tyr	Ile	275	280	285	
Asn	Asn	Glu	Gln	Val	Arg	Thr	Ala	Arg	Pro	Pro	Leu	Arg	Glu	Gln	Gln	290	295	300	
Phe	Asn	Ser	Thr	Ile	Arg	Val	Val	Ser	Thr	Leu	Pro	Ile	Ala	His	Gln	305	310	315	320
Asp	Trp	Leu	Arg	Gly	Lys	Glu	Phe	Lys	Cys	Lys	Val	His	Asn	Lys	Ala	325	330	335	
Leu	Pro	Ala	Pro	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	Arg	Gly	Gln	Pro	340	345	350	
Leu	Glu	Pro	Lys	Val	Tyr	Thr	Met	Gly	Pro	Pro	Arg	Glu	Glu	Leu	Ser	355	360	365	
Ser	Arg	Ser	Val	Ser	Leu	Thr	Cys	Met	Ile	Asn	Gly	Phe	Tyr	Pro	Ser	370	375	380	
Asp	Ile	Ser	Val	Glu	Trp	Glu	Lys	Asn	Gly	Lys	Ala	Glu	Asp	Asn	Tyr	385	390	395	400
Lys	Thr	Thr	Pro	Ala	Val	Leu	Asp	Ser	Asp	Gly	Ser	Tyr	Phe	Leu	Tyr	405	410	415	
Asn	Lys	Leu	Ser	Val	Pro	Thr	Ser	Glu	Trp	Gln	Arg	Gly	Asp	Val	Phe	420	425	430	
Thr	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr	Gln	Lys	435	440	445	
Ser	Ile	Ser	Arg	Ser	Pro	Gly	Lys									450	455		

<210> 61  
 <211> 1368  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> A synthetic M83 020B08H anti-CD83 heavy chain  
 sequence

<400> 61  
 atggagacag gcctgcgctg gcttctcctg gtcgctgtgc tcaaaggtgt ccagtgtcag 60  
 tcggtggagg agtccggggg tcgcctgggt acgcctggga caccctgac actcacctgc 120  
 acagtctctg gattctccct cagcagctac gacatgacct gggtcgcgcca ggctccaggg 180  
 aaggggctgg aatggatcgg aatcatttat gctagtggta ccacatacta cgcgaactgg 240  
 gcgaaaggcc gattcaccat ctccaaaacc tcgaccacgg tggatctgaa agtcaccagt 300  
 ccgacaatcg gggacacggc cacctatttc tgtgccagag agggggctgg tgttagtatg 360  
 accttgtggg gcccaggcac cctgggtcacc gtctcctcag ggcaacctaa ggctccatca 420  
 gtcttccccc tggcccccct ctgcggggac acaccctcta gcacggtgac cttgggctgc 480  
 ctggtcaaag gctacctccc ggagccagtg accgtgacct ggaactcggg caccctcacc 540  
 aatgggggtac gcaccttccc gtccgtccgg cagtcctcag gcctctactc gctgagcagc 600  
 gtgggtgagcg tgacctcaag cagccagccc gtcacctgca acgtggccca cccagccacc 660  
 aacaccaaag tggacaagac cgttgcgccc tcgacatgca gcaagcccac gtgcccacc 720  
 cctgaactcc tggggggacc gtctgtcttc atcttcccc caaaacccaa ggacaccctc 780  
 atgatctcac gcacccccga ggtcacatgc gtgggtgggg acgtgagcca ggatgacccc 840  
 gaggtgcagt tcacatggta cataaacaac gaggcaggtg gcaccgcccg gccgcccgcta 900  
 cgggagcagc agttcaacag cacgatccgc gtgggtcagca ccttccccat cgcgcaccag 960  
 gactggctga ggggcaagga gttcaagtgc aaagtccaca acaaggcact cccggccccc 1020  
 atcgagaaaa ccatctccaa agccagaggg cagcccctgg agccgaaggt ctacaccatg 1080  
 ggccttcccc gggaggagct gaggcagagg tcgggtcagcc tgacctgcat gatcaacggc 1140  
 ttctaccctt ccgacatctc ggtggagtgg gagaagaacg ggaaggcaga ggacaactac 1200  
 aagaccacgc cggcgtgct ggacagcgac ggctcctact tcctctacaa caagtctca 1260  
 gtgcccacga gtgagtggca gcggggcgac gtcttcacct gctccgtgat gcacgaggcc 1320  
 ttgcacaacc actacacgca gaagtccatc tcccgctctc cgggtaaa 1368

<210> 62  
 <211> 236  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> A synthetic M83 006G05L light chain sequence

<400> 62  
 Met Asp Met Arg Ala Pro Thr Gln Leu Leu Gly Leu Leu Leu Leu Trp  
 1 5 10 15  
 Leu Pro Gly Ala Arg Cys Ala Tyr Asp Met Thr Gln Thr Pro Ala Ser  
 20 25 30  
 Val Glu Val Ala Val Gly Gly Thr Val Ala Ile Lys Cys Gln Ala Ser  
 35 40 45  
 Gln Ser Val Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln  
 50 55 60  
 Pro Pro Lys Pro Leu Ile Tyr Glu Ala Ser Met Leu Ala Ala Gly Val  
 65 70 75 80  
 Ser Ser Arg Phe Lys Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr  
 85 90 95  
 Ile Ser Asp Leu Glu Cys Asp Asp Ala Ala Thr Tyr Tyr Cys Gln Gln  
 100 105 110  
 Gly Tyr Ser Ile Ser Asp Ile Asp Asn Ala Phe Gly Gly Gly Thr Glu  
 115 120 125  
 Val Val Val Lys Gly Asp Pro Val Ala Pro Thr Val Leu Leu Phe Pro  
 130 135 140

```

Pro Ser Ser Asp Glu Val Ala Thr Gly Thr Val Thr Ile Val Cys Val
145          150          155          160
Ala Asn Lys Tyr Phe Pro Asp Val Thr Val Thr Trp Glu Val Asp Gly
          165          170          175
Thr Thr Gln Thr Thr Gly Ile Glu Asn Ser Lys Thr Pro Gln Asn Ser
          180          185          190
Ala Asp Cys Thr Tyr Asn Leu Ser Ser Thr Leu Thr Leu Thr Ser Thr
          195          200          205
Gln Tyr Asn Ser His Lys Glu Tyr Thr Cys Lys Val Thr Gln Gly Thr
          210          215          220
Thr Ser Val Val Gln Ser Phe Ser Arg Lys Asn Cys
225          230          235

```

<210> 63  
 <211> 711  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> A synthetic M83 006G05L anti-CD83 light chain  
 sequence

```

<400> 63
atggacatga gggccccac tcaactgctg gggctcctgc tgctctggct cccaggtgcc      60
agatgtgcct atgatatgac ccagactcca gcctctgtgg aggtagctgt gggaggcaca      120
gtcgccatca agtgccaggc cagtcagagc gttagtagtt acttagcctg gtatcagcag      180
aaaccagggc agcctcccaa gcccctgata tacgaagcat ccattgctggc ggctgggggc      240
tcacgcgggt tcaaaggcag tggatctggg acagacttca ctctcaccat cagcgacctg      300
gagtgtgacg atgctgccac ttactattgt caacagggtt attctatcag tgatattgat      360
aatgctttcg gcggaggggc cgaggtggtg gtcaaagggt atccagttgc acctactgtc      420
ctcctcttcc caccatctag cgatgaggtg gcaactggaa cagtcaccat cgtgtgtgtg      480
gcgaataaat actttcccgga tgtcaccgtc acctggggagg tggatggcac caccctcagc      540
actggcatcg agaacagtaa aacaccgcag aattctgcag attgtacct caacctcagc      600
agcactctga cactgaccag cacacagtac aacagccaca aagagtacac ctgcaagggtg      660
accaggggca cgacctcagt cgtccagagc ttcagtagga agaactgtta a          711

```

<210> 64  
 <211> 459  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> A synthetic M83 006G05L heavy chain sequence

```

<400> 64
Met Glu Thr Gly Leu Arg Trp Leu Leu Leu Val Ala Val Leu Lys Gly
 1          5          10          15
Val Gln Cys Gln Ser Val Glu Glu Ser Gly Gly Arg Leu Val Ser Pro
          20          25          30
Gly Thr Pro Leu Thr Leu Thr Cys Thr Ala Ser Gly Phe Ser Leu Ser
          35          40          45
Ser Tyr Asp Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu
          50          55          60
Tyr Ile Gly Ile Ile Ser Ser Ser Gly Ser Thr Tyr Tyr Ala Ser Trp
65          70          75          80
Ala Lys Gly Arg Phe Thr Ile Ser Lys Thr Ser Thr Thr Val Asp Leu
          85          90          95
Glu Val Thr Ser Leu Thr Thr Glu Asp Thr Ala Thr Tyr Phe Cys Ser
          100          105          110
Arg Glu His Ala Gly Tyr Ser Gly Asp Thr Gly His Leu Trp Gly Pro
          115          120          125

```

Gly	Thr	Leu	Val	Thr	Val	Ser	Ser	Gly	Gln	Pro	Lys	Ala	Pro	Ser	Val
130						135					140				
Phe	Pro	Leu	Ala	Pro	Cys	Cys	Gly	Asp	Thr	Pro	Ser	Ser	Thr	Val	Thr
145					150					155					160
Leu	Gly	Cys	Leu	Val	Lys	Gly	Tyr	Leu	Pro	Glu	Pro	Val	Thr	Val	Thr
				165					170					175	
Trp	Asn	Ser	Gly	Thr	Leu	Thr	Asn	Gly	Val	Arg	Thr	Phe	Pro	Ser	Val
			180					185					190		
Arg	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Ser	Val	Thr
		195					200					205			
Ser	Ser	Ser	Gln	Pro	Val	Thr	Cys	Asn	Val	Ala	His	Pro	Ala	Thr	Asn
		210				215					220				
Thr	Lys	Val	Asp	Lys	Thr	Val	Ala	Pro	Ser	Thr	Cys	Ser	Lys	Pro	Thr
225					230					235					240
Cys	Pro	Pro	Pro	Glu	Leu	Leu	Gly	Gly	Pro	Ser	Val	Phe	Ile	Phe	Pro
				245					250					255	
Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr
			260					265					270		
Cys	Val	Val	Val	Asp	Val	Ser	Gln	Asp	Asp	Pro	Glu	Val	Gln	Phe	Thr
		275					280					285			
Trp	Tyr	Ile	Asn	Asn	Glu	Gln	Val	Arg	Thr	Ala	Arg	Pro	Pro	Leu	Arg
	290					295					300				
Glu	Gln	Gln	Phe	Asn	Ser	Thr	Ile	Arg	Val	Val	Ser	Thr	Leu	Pro	Ile
305					310					315					320
Ala	His	Gln	Asp	Trp	Leu	Arg	Gly	Lys	Glu	Phe	Lys	Cys	Lys	Val	His
			325						330					335	
Asn	Lys	Ala	Leu	Pro	Ala	Pro	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	Arg
		340						345					350		
Gly	Gln	Pro	Leu	Glu	Pro	Lys	Val	Tyr	Thr	Met	Gly	Pro	Pro	Arg	Glu
		355					360					365			
Glu	Leu	Ser	Ser	Arg	Ser	Val	Ser	Leu	Thr	Cys	Met	Ile	Asn	Gly	Phe
	370					375					380				
Tyr	Pro	Ser	Asp	Ile	Ser	Val	Glu	Trp	Glu	Lys	Asn	Gly	Lys	Ala	Glu
385					390					395					400
Asp	Asn	Tyr	Lys	Thr	Thr	Pro	Ala	Val	Leu	Asp	Ser	Asp	Gly	Ser	Tyr
			405						410					415	
Phe	Leu	Tyr	Asn	Lys	Leu	Ser	Val	Pro	Thr	Ser	Glu	Trp	Gln	Arg	Gly
			420					425					430		
Asp	Val	Phe	Thr	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His	Asn	His	Tyr
	435						440					445			
Thr	Gln	Lys	Ser	Ile	Ser	Arg	Ser	Pro	Gly	Lys					
450						455									

<210> 65

<211> 1377

<212> DNA

<213> Artificial Sequence

<220>

<223> A synthetic M83 006G05L anti-CD83 heavy chain sequence

<400> 65

atggagacag	gcctgcgctg	gcttctcctg	gtcgctgtgc	tcaaaggtgt	ccagtgtcag	60
tcgggtggagg	agtcgggggg	tcgcctgggc	tcgcctggga	caccctgac	actcacctgc	120
acagcctctg	gattctccct	cagtagctac	gacatgagct	gggtccgcca	ggctccaggg	180
aaggggctgg	aatacatcgg	aatcattagt	agtagtggtg	gcacatacta	cgcgagctgg	240
gcgaaaggcc	gattcaccat	ctccaaaacc	tcgaccacgg	tggatctgga	agtgaccagt	300
ctgacaaccg	aggacacggc	cacctatttc	tgtagtagag	aacatgctgg	ttatagtggg	360
gatacgggtc	acttgtgggg	cccaggcacc	ctgggtcaccg	tctcctcgga	gcaacctaag	420

```

gctccatcag tcttcccact ggccccctgc tgcgggggaca caccctctag cacggtgacc 480
ttggggtgcc tgggtcaaagg ctacctcccg gagccagtga ccgtgacctg gaactcgggc 540
accctcacca atgggggtacg caccctcccg tccgtccggc agtcctcagg cctctactcg 600
ctgagcagcg tgggtgagcgt gacctcaagc agccagcccg tcacctgcaa cgtggcccac 660
ccagccacca acaccaaagt ggacaagacc gttgcgcctt cgacatgcag caagcccacg 720
tgcccccccc ctgaactcct ggggggaccg tctgtcttca tcttcccccc aaaacccaag 780
gacacctca tgatctcacg cccccccgag gtcacatgcg tgggtggtgga cgtgagccag 840
gatgaccccg aggtgcagtt cacatggtac ataaacaacg agcaggtgcg caccgcccgg 900
ccgccgctac gggagcagca gttcaacagc acgatccgcg tggtcagcac cctccccatc 960
gcgccaccagg actgggtgag gggcaaggag ttcaagtgc aagtccacaa caaggcactc 1020
ccggccccca tcgagaaaac catctccaaa gccagagggc agcccctgga gccgaaggtc 1080
tacaccatgg gccctccccg ggaggagctg agcagcaggt cggtcagcct gacctgcatg 1140
atcaacggct tctacccttc cgacatctcg gtggagtggg agaagaacgg gaaggcagag 1200
gacaactaca agaccacgcc ggccgtgctg gacagcgacg gctcctactt cctctacaac 1260
aagctctcag tgcccacgag tgagtggcag cggggcgacg tcttcacctg ctccgtgatg 1320
cacgaggcct tgcacaacca ctacacgcag aagtccatct cccgctctcc gggtaaaa 1377

```

<210> 66

<211> 150

<212> PRT

<213> Artificial Sequence

<220>

<223> A synthetic anti-CD83 heavy chain variable region  
sequence

<400> 66

```

Met Glu Thr Gly Leu Arg Trp Leu Leu Leu Val Ala Val Leu Lys Gly
1          5          10          15
Val Gln Cys Gln Ser Val Glu Glu Ser Gly Gly Arg Leu Val Thr Pro
20          25          30
Gly Thr Pro Leu Thr Leu Thr Cys Thr Val Ser Gly Phe Thr Ile Ser
35          40          45
Asp Tyr Asp Leu Ser Trp Val Arg Gln Ala Pro Gly Glu Gly Leu Lys
50          55          60
Tyr Ile Gly Phe Ile Ala Ile Asp Gly Asn Pro Tyr Tyr Ala Thr Trp
65          70          75          80
Ala Lys Gly Arg Phe Thr Ile Ser Lys Thr Ser Thr Thr Val Asp Leu
85          90          95
Lys Ile Thr Ala Pro Thr Thr Glu Asp Thr Ala Thr Tyr Phe Cys Ala
100         105         110
Arg Gly Ala Gly Asp Leu Trp Gly Pro Gly Thr Leu Val Thr Val Ser
115         120         125
Ser Gly Gln Pro Lys Ala Pro Ser Val Phe Pro Leu Ala Pro Cys Cys
130         135         140
Gly Asp Thr Pro Ser Ser
145         150

```

<210> 67

<211> 152

<212> PRT

<213> Artificial Sequence

<220>

<223> A synthetic anti-CD83 heavy chain variable region  
sequence

<400> 67

```

Met Glu Thr Gly Leu Arg Trp Leu Leu Leu Val Ala Val Leu Lys Gly
1          5          10          15
Val His Cys Gln Ser Val Glu Glu Ser Gly Gly Arg Leu Val Thr Pro
20          25          30

```

Gly Thr Pro Leu Thr Leu Thr Cys Thr Ala Ser Gly Phe Ser Arg Ser  
           35                  40          45  
 Ser Tyr Asp Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu  
       50                  55          60  
 Trp Val Gly Val Ile Ser Thr Ala Tyr Asn Ser His Tyr Ala Ser Trp  
 65                  70          75          80  
 Ala Lys Gly Arg Phe Thr Ile Ser Arg Thr Ser Thr Thr Val Asp Leu  
                   85          90          95  
 Lys Met Thr Ser Leu Thr Thr Glu Asp Thr Ala Thr Tyr Phe Cys Ala  
           100          105          110  
 Arg Gly Gly Ser Trp Leu Asp Leu Trp Gly Gln Gly Thr Leu Val Thr  
       115          120          125  
 Val Ser Ser Gly Gln Pro Lys Ala Pro Ser Val Phe Pro Leu Ala Pro  
       130          135          140  
 Cys Cys Gly Asp Thr Pro Ser Ser  
 145                  150

<210> 68  
 <211> 149  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> A synthetic anti-CD83 light chain variable region  
           sequence

<400> 68  
 Met Asp Thr Arg Ala Pro Thr Gln Leu Leu Gly Leu Leu Leu Leu Trp  
   1                  5          10          15  
 Leu Pro Gly Ala Arg Cys Ala Asp Val Val Met Thr Gln Thr Pro Ala  
           20          25          30  
 Ser Val Ser Ala Ala Val Gly Gly Thr Val Thr Ile Asn Cys Gln Ser  
       35          40          45  
 Ser Lys Asn Val Tyr Asn Asn Asn Trp Leu Ser Trp Phe Gln Gln Lys  
       50          55          60  
 Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Tyr Ala Ser Thr Leu Ala  
 65                  70          75          80  
 Ser Gly Val Pro Ser Arg Phe Arg Gly Ser Gly Ser Gly Thr Gln Phe  
                   85          90          95  
 Thr Leu Thr Ile Ser Asp Val Gln Cys Asp Asp Ala Ala Thr Tyr Tyr  
           100          105          110  
 Cys Ala Gly Asp Tyr Ser Ser Ser Ser Asp Asn Gly Phe Gly Gly Gly  
       115          120          125  
 Thr Glu Val Val Val Lys Gly Asp Pro Val Ala Pro Thr Val Leu Leu  
       130          135          140  
 Phe Pro Pro Ser Ser  
 145

<210> 69  
 <211> 149  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <221> SITE  
 <222> (1)...(149)  
 <223> Xaa = any amino acid

<220>  
 <223> A synthetic anti-CD83 light chain variable region  
           sequence

<400> 69

```
Met Asp Xaa Arg Ala Pro Thr Gln Leu Leu Gly Leu Leu Leu Leu Trp
 1          5          10          15
Leu Pro Gly Ala Arg Cys Ala Leu Val Met Thr Gln Thr Pro Ala Ser
          20          25          30
Val Ser Ala Ala Val Gly Gly Thr Val Thr Ile Asn Cys Gln Ser Ser
          35          40          45
Gln Ser Val Tyr Asp Asn Asp Glu Leu Ser Trp Tyr Gln Gln Lys Pro
          50          55          60
Gly Gln Pro Pro Lys Leu Leu Ile Tyr Leu Ala Ser Lys Leu Ala Ser
65          70          75          80
Gly Val Pro Ser Arg Phe Lys Gly Ser Gly Ser Gly Thr Gln Phe Ala
          85          90          95
Leu Thr Ile Ser Gly Val Gln Cys Asp Asp Ala Ala Thr Tyr Tyr Cys
          100          105          110
Gln Ala Thr His Tyr Ser Ser Asp Trp Tyr Leu Thr Phe Gly Gly Gly
          115          120          125
Thr Glu Val Val Val Lys Gly Asp Pro Val Ala Pro Thr Val Leu Leu
          130          135          140
Phe Pro Pro Ser Ser
145
```

<210> 70

<211> 240

<212> PRT

<213> Artificial Sequence

<220>

<223> A synthetic 96G08 light chain sequence

<400> 70

```
Met Asp Thr Arg Ala Pro Thr Gln Leu Leu Gly Leu Leu Leu Leu Trp
 1          5          10          15
Leu Pro Gly Ala Thr Phe Ala Gln Val Leu Thr Gln Thr Ala Ser Pro
          20          25          30
Val Ser Ala Pro Val Gly Gly Thr Val Thr Ile Asn Cys Gln Ser Ser
          35          40          45
Gln Ser Val Tyr Asn Asn Asp Phe Leu Ser Trp Tyr Gln Gln Lys Pro
          50          55          60
Gly Gln Pro Pro Lys Leu Leu Ile Tyr Tyr Ala Ser Thr Leu Ala Ser
65          70          75          80
Gly Val Pro Ser Arg Phe Lys Gly Ser Gly Ser Gly Thr Gln Phe Thr
          85          90          95
Leu Thr Ile Ser Asp Leu Glu Cys Asp Asp Ala Ala Thr Tyr Tyr Cys
          100          105          110
Thr Gly Thr Tyr Gly Asn Ser Ala Trp Tyr Glu Asp Ala Phe Gly Gly
          115          120          125
Gly Thr Glu Val Val Val Lys Arg Thr Pro Val Ala Pro Thr Val Leu
          130          135          140
Leu Phe Pro Pro Ser Ser Ala Glu Leu Ala Thr Gly Thr Ala Thr Ile
145          150          155          160
Val Cys Val Ala Asn Lys Tyr Phe Pro Asp Gly Thr Val Thr Trp Lys
          165          170          175
Val Asp Gly Ile Thr Gln Ser Ser Gly Ile Asn Asn Ser Arg Thr Pro
          180          185          190
Gln Asn Ser Ala Asp Cys Thr Tyr Asn Leu Ser Ser Thr Leu Thr Leu
          195          200          205
Ser Ser Asp Glu Tyr Asn Ser His Asp Glu Tyr Thr Cys Gln Val Ala
          210          215          220
Gln Asp Ser Gly Ser Pro Val Val Gln Ser Phe Ser Arg Lys Ser Cys
225          230          235          240
```

<210> 71  
 <211> 13  
 <212> PRT  
 <213> Oryctolagus cuniculus

<400> 71  
 Gln Ser Ser Gln Ser Val Tyr Asn Asn Asp Phe Leu Ser  
 1 5 10

<210> 72  
 <211> 7  
 <212> PRT  
 <213> Oryctolagus cuniculus

<400> 72  
 Tyr Ala Ser Thr Leu Ala Ser  
 1 5

<210> 73  
 <211> 13  
 <212> PRT  
 <213> Oryctolagus cuniculus

<400> 73  
 Thr Gly Thr Tyr Gly Asn Ser Ala Trp Tyr Glu Asp Ala  
 1 5 10

<210> 74  
 <211> 723  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> A synthetic 96G08 anti-CD83 light chain sequence

<400> 74  
 atggacacga gggccccac tcagctgctg gggctcctgc tgctctggct cccaggtgcc 60  
 acatttgcg aagtgctgac ccagactgca tcgcccgtgt ctgcacctgt gggaggcaca 120  
 gtcaccatca attgccagtc cagtcagagt gtttataata acgacttctt atcctgggtat 180  
 cagcagaaac cagggcagcc tcccaaactc ctgatctatt atgcatccac tctggcatct 240  
 ggggtcccat cccggttcaa aggcagtgga tctgggacac agttcactct caccatcagc 300  
 gacctggagt gtgacgatgc tgccacttac tactgtacag gcacttatgg taatagtgtc 360  
 tggtagcagg atgctttcgg cggagggacc gaggtgggtg tcaaactgtac gccagttgca 420  
 cctactgtcc tcctcttccc accatctagc gctgagctgg caactggaac agccaccatc 480  
 gtgtgcgtgg cgaataaata ctttcccgat ggcaccgtca cctggaaggt ggatggcatc 540  
 acccaaagca gcggcatcaa taacagtaga acaccgcaga attctgcaga ttgtacctac 600  
 aacctcagca gtactctgac actgagcagc gacgagtaca acagccacga cgagtacacc 660  
 tgccaggtgg cccaggactc aggctcaccg gtcgtccaga gcttcagtag gaagagctgt 720  
 tag 723

<210> 75  
 <211> 25  
 <212> DNA  
 <213> Oryctolagus cuniculus

<400> 75  
 cagtcagtc agagtgttta taata 25



<210> 76  
 <211> 20  
 <212> DNA  
 <213> Oryctolagus cuniculus

<400> 76  
 atgcatccac tctggcatct

20

<210> 77  
 <211> 25  
 <212> DNA  
 <213> Oryctolagus cuniculus

<400> 77  
 acaggcactt atggtaatag tgctt

25

<210> 78  
 <211> 456  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> A synthetic 96G08 heavy chain sequence

<400> 78  
 Met Glu Thr Gly Leu Arg Trp Leu Leu Leu Val Ala Val Leu Lys Gly  
 1 5 10 15  
 Val Gln Cys Gln Ser Val Glu Glu Ser Gly Gly Arg Leu Val Thr Pro  
 20 25 30  
 Gly Thr Pro Leu Thr Leu Thr Cys Thr Val Ser Gly Ile Asp Leu Ser  
 35 40 45  
 Ser Asp Gly Ile Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu  
 50 55 60  
 Trp Ile Gly Ile Ile Ser Ser Gly Gly Asn Thr Tyr Tyr Ala Ser Trp  
 65 70 75 80  
 Ala Lys Gly Arg Phe Thr Ile Ser Arg Thr Ser Thr Thr Val Asp Leu  
 85 90 95  
 Lys Met Thr Ser Leu Thr Thr Glu Asp Thr Ala Thr Tyr Phe Cys Ala  
 100 105 110  
 Arg Val Val Gly Gly Thr Tyr Ser Ile Trp Gly Gln Gly Thr Leu Val  
 115 120 125  
 Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Tyr Pro Leu Ala  
 130 135 140  
 Pro Gly Ser Ala Ala Gln Thr Asn Ser Met Val Thr Leu Gly Cys Leu  
 145 150 155 160  
 Val Lys Gly Tyr Phe Pro Glu Pro Val Thr Val Thr Trp Asn Ser Gly  
 165 170 175  
 Ser Leu Ser Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Asp  
 180 185 190  
 Leu Tyr Thr Leu Ser Ser Ser Val Thr Val Pro Ser Ser Thr Trp Pro  
 195 200 205  
 Ser Glu Thr Val Thr Cys Asn Val Ala His Pro Ala Ser Ser Thr Lys  
 210 215 220  
 Val Asp Lys Lys Ile Val Pro Arg Asp Cys Gly Cys Lys Pro Cys Ile  
 225 230 235 240  
 Cys Thr Val Pro Glu Val Ser Ser Val Phe Ile Phe Pro Pro Lys Pro  
 245 250 255  
 Lys Asp Val Leu Thr Ile Thr Leu Thr Pro Lys Val Thr Cys Val Val  
 260 265 270  
 Val Asp Ile Ser Lys Asp Asp Pro Glu Val Gln Phe Ser Trp Phe Val  
 275 280 285

Asp	Asp	Val	Glu	Val	His	Thr	Ala	Gln	Thr	Gln	Pro	Arg	Glu	Glu	Gln
290						295					300				
Phe	Asn	Ser	Thr	Phe	Arg	Ser	Val	Ser	Glu	Leu	Pro	Ile	Met	His	Gln
305					310					315					320
Asp	Trp	Leu	Asn	Gly	Lys	Glu	Phe	Lys	Cys	Arg	Val	Asn	Ser	Ala	Ala
			325						330					335	
Phe	Pro	Ala	Pro	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Thr	Lys	Gly	Arg	Pro
		340					345						350		
Lys	Ala	Pro	Gln	Val	Tyr	Thr	Ile	Pro	Pro	Pro	Lys	Glu	Gln	Met	Ala
	355					360						365			
Lys	Asp	Lys	Val	Ser	Leu	Thr	Cys	Met	Ile	Thr	Asp	Phe	Phe	Pro	Glu
370						375					380				
Asp	Ile	Thr	Val	Glu	Trp	Gln	Trp	Asn	Gly	Gln	Pro	Ala	Glu	Asn	Tyr
385				390						395					400
Lys	Asn	Thr	Gln	Pro	Ile	Met	Asp	Thr	Asp	Gly	Ser	Tyr	Phe	Val	Tyr
			405						410					415	
Ser	Lys	Leu	Asn	Val	Gln	Lys	Ser	Asn	Trp	Glu	Ala	Gly	Asn	Thr	Phe
			420					425					430		
Thr	Cys	Ser	Val	Leu	His	Glu	Gly	Leu	His	Asn	His	His	Thr	Glu	Lys
	435						440					445			
Ser	Leu	Ser	His	Ser	Pro	Gly	Lys								
450						455									

<210> 79  
 <211> 5  
 <212> PRT  
 <213> Oryctolagus cuniculus

<400> 79  
 Ser Asp Gly Ile Ser  
 1 5

<210> 80  
 <211> 16  
 <212> PRT  
 <213> Oryctolagus cuniculus

<400> 80  
 Ile Ile Ser Ser Gly Gly Asn Thr Tyr Tyr Ala Ser Trp Ala Lys Gly  
 1 5 10 15

<210> 81  
 <211> 8  
 <212> PRT  
 <213> Oryctolagus cuniculus

<400> 81  
 Val Val Gly Gly Thr Tyr Ser Ile  
 1 5

<210> 82  
 <211> 1371  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> A synthetic 96G08 anti-CD83 heavy chain sequence

<400> 82  
 atggagactg ggctgcgctg gcttctcctg gtcgctgtgc tcaaagggtg ccagtgtcag 60  
 tcggtggagg agtccggggg tcgcctgggc acacctggga caccctgac actcacctgc 120



Ser Gln Ser Val Tyr Gly Asn Asn Glu Leu Ser Trp Tyr Gln Gln Lys  
 50 55 60  
 Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Gln Ala Ser Ser Leu Ala  
 65 70 75 80  
 Ser Gly Val Pro Ser Arg Phe Lys Gly Ser Gly Ser Gly Thr Gln Phe  
 85 90 95  
 Thr Leu Thr Ile Ser Asp Leu Glu Cys Asp Asp Ala Ala Thr Tyr Tyr  
 100 105 110  
 Cys Leu Gly Glu Tyr Ser Ile Ser Ala Asp Asn His Phe Gly Gly Gly  
 115 120 125  
 Thr Glu Val Val Val Lys Arg Thr Pro Val Ala Pro Thr Val Leu Leu  
 130 135 140  
 Phe Pro Pro Ser Ser Ala Glu Leu Ala Thr Gly Thr Ala Thr Ile Val  
 145 150 155 160  
 Cys Val Ala Asn Lys Tyr Phe Pro Asp Gly Thr Val Thr Trp Lys Val  
 165 170 175  
 Asp Gly Ile Thr Gln Ser Ser Gly Ile Asn Asn Ser Arg Thr Pro Gln  
 180 185 190  
 Asn Ser Ala Asp Cys Thr Tyr Asn Leu Ser Ser Thr Leu Thr Leu Ser  
 195 200 205  
 Ser Asp Glu Tyr Asn Ser His Asp Glu Tyr Thr Cys Gln Val Ala Gln  
 210 215 220  
 Asp Ser Gly Ser Pro Val Val Gln Ser Phe Ser Arg Lys Ser Cys  
 225 230 235

<210> 87  
 <211> 13  
 <212> PRT  
 <213> Oryctolagus cuniculus

<400> 87  
 Gln Ser Ser Gln Ser Val Tyr Gly Asn Asn Glu Leu Ser  
 1 5 10

<210> 88  
 <211> 7  
 <212> PRT  
 <213> Oryctolagus cuniculus

<400> 88  
 Gln Ala Ser Ser Leu Ala Ser  
 1 5

<210> 89  
 <211> 11  
 <212> PRT  
 <213> Oryctolagus cuniculus

<400> 89  
 Leu Gly Glu Tyr Ser Ile Ser Ala Asp Asn His  
 1 5 10

<210> 90  
 <211> 720  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> A synthetic 95F04 anti-CD83 light chain sequence

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<400> 90
atggacacga gggcccccac tcagctgctg gggctcctgc tgctctggct cccaggtgcc      60
acatttgccc aagccgtggt gaccagact acatcgcccg tgtctgcacc tgtgggaggc      120
acagtcacca tcaattgcca gtccagtcag agtggttatg gtaacaacga attatcctgg      180
tatcagcaga aaccagggca gcctcccaag ctctgatct accaggcatc cagcctggca      240
tctgggggtcc catcgcggtt caaaggcagt ggatctggga cacagttcac tctcaccatc      300
agcgacctgg agtgtgacga tgctgccact tactactgtc taggcgaata tagcattagt      360
gctgataatc atttcggcgg agggaccgag gtgggtgtca aacgtacgcc agttgcacct      420
actgtcctcc tcttcccacc atctagcgct gagctggcaa ctggaacagc caccatcgtg      480
tgcgtggcga ataaataactt tcccgatggc accgtcacct ggaaggtgga tggcatcacc      540
caaagcagcg gcatcaataa cagtagaaca ccgcagaatt ctgcagattg tacctacaac      600
ctcagcagta ctctgacact gagcagcgac gagtacaaca gccacgacga gtacacctgc      660
caggtggccc aggactcagg ctcaccggtc gtccagagct tcagtaggaa gagctgttag      720

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<210> 91

<211> 460

<212> PRT

<213> Artificial Sequence

<220>

<223> A synthetic 95F04 heavy chain sequence

<400> 91

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Met Glu Thr Gly Leu Arg Trp Leu Leu Leu Val Ala Val Leu Lys Gly
 1           5           10           15
Val Gln Cys Gln Ser Val Glu Glu Ser Gly Gly Arg Leu Val Thr Pro
          20          25          30
Gly Thr Pro Leu Thr Leu Thr Cys Thr Val Ser Gly Ile Asp Leu Ser
          35          40          45
Ser Asn Ala Met Ile Trp Val Arg Gln Ala Pro Arg Glu Gly Leu Glu
          50          55          60
Trp Ile Gly Ala Met Asp Ser Asn Ser Arg Thr Tyr Tyr Ala Thr Trp
65          70          75          80
Ala Lys Gly Arg Phe Thr Ile Ser Arg Thr Ser Ser Ile Thr Val Asp
          85          90          95
Leu Lys Ile Thr Ser Pro Thr Thr Glu Asp Thr Ala Thr Tyr Phe Cys
          100         105         110
Ala Arg Gly Asp Gly Gly Ser Ser Asp Tyr Thr Glu Met Trp Gly Pro
          115         120         125
Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
          130         135         140
Tyr Pro Leu Ala Pro Gly Ser Ala Ala Gln Thr Asn Ser Met Val Thr
145         150         155         160
Leu Gly Cys Leu Val Lys Gly Tyr Phe Pro Glu Pro Val Thr Val Thr
          165         170         175
Trp Asn Ser Gly Ser Leu Ser Ser Gly Val His Thr Phe Pro Ala Val
          180         185         190
Leu Gln Ser Asp Leu Tyr Thr Leu Ser Ser Ser Val Thr Val Pro Ser
          195         200         205
Ser Thr Trp Pro Ser Glu Thr Val Thr Cys Asn Val Ala His Pro Ala
          210         215         220
Ser Ser Thr Lys Val Asp Lys Lys Ile Val Pro Arg Asp Cys Gly Cys
225         230         235         240
Lys Pro Cys Ile Cys Thr Val Pro Glu Val Ser Ser Val Phe Ile Phe
          245         250         255
Pro Pro Lys Pro Lys Asp Val Leu Thr Ile Thr Leu Thr Pro Lys Val
          260         265         270
Thr Cys Val Val Val Asp Ile Ser Lys Asp Asp Pro Glu Val Gln Phe
          275         280         285
Ser Trp Phe Val Asp Asp Val Glu Val His Thr Ala Gln Thr Gln Pro
290         295         300

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Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg Ser Val Ser Glu Leu Pro  
 305 310 315 320  
 Ile Met His Gln Asp Trp Leu Asn Gly Lys Glu Phe Lys Cys Arg Val  
 325 330 335  
 Asn Ser Ala Ala Phe Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr  
 340 345 350  
 Lys Gly Arg Pro Lys Ala Pro Gln Val Tyr Thr Ile Pro Pro Pro Lys  
 355 360 365  
 Glu Gln Met Ala Lys Asp Lys Val Ser Leu Thr Cys Met Ile Thr Asp  
 370 375 380  
 Phe Phe Pro Glu Asp Ile Thr Val Glu Trp Gln Trp Asn Gly Gln Pro  
 385 390 395 400  
 Ala Glu Asn Tyr Lys Asn Thr Gln Pro Ile Met Asp Thr Asp Gly Ser  
 405 410 415  
 Tyr Phe Val Tyr Ser Lys Leu Asn Val Gln Lys Ser Asn Trp Glu Ala  
 420 425 430  
 Gly Asn Thr Phe Thr Cys Ser Val Leu His Glu Gly Leu His Asn His  
 435 440 445  
 His Thr Glu Lys Ser Leu Ser His Ser Pro Gly Lys  
 450 455 460

<210> 92  
 <211> 5  
 <212> PRT  
 <213> Oryctolagus cuniculus

<400> 92  
 Ser Asn Ala Met Ile  
 1 5

<210> 93  
 <211> 16  
 <212> PRT  
 <213> Oryctolagus cuniculus

<400> 93  
 Ala Met Asp Ser Asn Ser Arg Thr Tyr Tyr Ala Thr Trp Ala Lys Gly  
 1 5 10 15

<210> 94  
 <211> 11  
 <212> PRT  
 <213> Oryctolagus cuniculus

<400> 94  
 Gly Asp Gly Gly Ser Ser Asp Tyr Thr Glu Met  
 1 5 10

<210> 95  
 <211> 1383  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> A synthetic 95F04 anti-CD83 heavy chain sequence

<400> 95  
 atggagactg ggctgcgctg gcttctcctg gtcgctgtgc tcaaaggtgt ccagtgtcag 60  
 tcggtggagg agtccggggg tcgcctgggc acgcctggga caccctgac actcacctgc 120  
 acagtctctg gaatcgacct cagtagcaat gcaatgatct ggggccgcca ggctccaagg 180  
 gaggggctgg aatggatcgg agccatggat agtaatagta ggacgtacta cgcgacctgg 240  
 gcgaaaggcc gattcaccat ctccagaacc tcgtcgatta cgggtgatct gaaaatcacc 300

agtccgacaa	ccgaggacac	ggccacctat	ttctgtgcc	gaggggatgg	tggcagtagt	360
gattatacag	agatgtgggg	cccagggacc	ctcgtcaccc	tctcgagcgc	ttctacaaag	420
ggcccatctg	tctatccact	ggcccttgga	tctgctgccc	aaactaactc	catggtgacc	480
ctgggatgcc	tggtcaaggg	ctatttccct	gagccagtga	cagtgaacctg	gaactctgga	540
tccctgtcca	gcggtgtgca	caccttccca	gctgtcctgc	agtctgacct	ctacactctg	600
agcagctcag	tgactgtccc	ctccagcacc	tgccccagcg	agaccgtcac	ctgcaacggt	660
gccaccccg	ccagcagcac	caaggtggac	aagaaaattg	tgcccaggga	ttgtggttgt	720
aagccttgca	tatgtacagt	cccagaagta	tcattctgtct	tcattcttccc	cccaaagccc	780
aaggatgtgc	tcaccattac	tctgactcct	aaggtcacgt	gtgttggtgt	agacatcagc	840
aaggatgatc	ccgaggtcca	gttcagctgg	tttgtagatg	atgtggaggt	gcacacagct	900
cagacgcaac	cccgggagga	gcagttcaac	agcactttcc	gctcagtcag	tgaacttccc	960
atcatgcacc	aggactggct	caatggcaag	gagttcaa	gcagggtcaa	cagtgcagct	1020
ttccctgccc	ccatcgagaa	aaccatctcc	aaaaccaaag	gcagaccgaa	ggctccacag	1080
gtgtacacca	ttccacctcc	caaggagcag	atggccaagg	ataaagtcag	tctgacctgc	1140
atgataacag	acttcttccc	tgaagacatt	actgtggagt	ggcagtgga	tgggcagcca	1200
gcggaagact	acaagaacac	tcagcccatc	atggacacag	atggctctta	cttcgtctac	1260
agcaagctca	atgtgcagaa	gagcaactgg	gaggcaggaa	atactttcac	ctgctctgtg	1320
ttacatgagg	gcctgcacaa	ccaccatact	gagaagagcc	tctccctactc	tcctggtaaa	1380
tga						1383

<210> 96

<211> 1383

<212> DNA

<213> Artificial Sequence

<220>

<223> A synthetic 95F04 anti-CD83 light chain sequence

<400> 96

atggagactg	ggctgcgctg	gcttctcctg	gtcgtgtgtc	tcaaaggtgt	ccagtgtcag	60
tcggtggagg	agtccggggg	tcgcctggtc	acgcctggga	cacccttgac	actcacctgc	120
acagtctctg	gaatcgacct	cagtagcaat	gcaatgatct	gggtccgcca	ggctccaagg	180
gaggggctgg	aatggatcgg	agccatggat	agtaatagta	ggacgtacta	cgcgacctgg	240
gcgaaaggcc	gattcaccat	ctccagaacc	tcgtcgatta	cggtggatct	gaaaatcacc	300
agtccgacaa	ccgaggacac	ggccacctat	ttctgtgcc	gaggggatgg	tggcagtagt	360
gattatacag	agatgtgggg	cccagggacc	ctcgtcaccc	tctcgagcgc	ttctacaaag	420
ggcccatctg	tctatccact	ggcccttgga	tctgctgccc	aaactaactc	catggtgacc	480
ctgggatgcc	tggtcaaggg	ctatttccct	gagccagtga	cagtgaacctg	gaactctgga	540
tccctgtcca	gcggtgtgca	caccttccca	gctgtcctgc	agtctgacct	ctacactctg	600
agcagctcag	tgactgtccc	ctccagcacc	tgccccagcg	agaccgtcac	ctgcaacggt	660
gccaccccg	ccagcagcac	caaggtggac	aagaaaattg	tgcccaggga	ttgtggttgt	720
aagccttgca	tatgtacagt	cccagaagta	tcattctgtct	tcattcttccc	cccaaagccc	780
aaggatgtgc	tcaccattac	tctgactcct	aaggtcacgt	gtgttggtgt	agacatcagc	840
aaggatgatc	ccgaggtcca	gttcagctgg	tttgtagatg	atgtggaggt	gcacacagct	900
cagacgcaac	cccgggagga	gcagttcaac	agcactttcc	gctcagtcag	tgaacttccc	960
atcatgcacc	aggactggct	caatggcaag	gagttcaa	gcagggtcaa	cagtgcagct	1020
ttccctgccc	ccatcgagaa	aaccatctcc	aaaaccaaag	gcagaccgaa	ggctccacag	1080
gtgtacacca	ttccacctcc	caaggagcag	atggccaagg	ataaagtcag	tctgacctgc	1140
atgataacag	acttcttccc	tgaagacatt	actgtggagt	ggcagtgga	tgggcagcca	1200
gcggaagact	acaagaacac	tcagcccatc	atggacacag	atggctctta	cttcgtctac	1260
agcaagctca	atgtgcagaa	gagcaactgg	gaggcaggaa	atactttcac	ctgctctgtg	1320
ttacatgagg	gcctgcacaa	ccaccatact	gagaagagcc	tctccctactc	tcctggtaaa	1380
tga						1383

<210> 97

<211> 107

<212> PRT

<213> Homo sapiens

<400> 97

Pro	Glu	Val	Lys	Val	Ala	Cys	Ser	Glu	Asp	Val	Asp	Leu	Pro	Cys	Thr
1				5					10					15	

Ala Pro Trp Asp Pro Gln Val Pro Tyr Thr Val Ser Trp Val Lys Leu  
20 25 30  
Leu Glu Gly Gly Glu Glu Arg Met Glu Thr Pro Gln Glu Asp His Leu  
35 40 45  
Arg Gly Gln His Tyr His Gln Lys Gly Gln Asn Gly Ser Phe Asp Ala  
50 55 60  
Pro Asn Glu Arg Pro Tyr Ser Leu Lys Ile Arg Asn Thr Thr Ser Cys  
65 70 75 80  
Asn Ser Gly Thr Tyr Arg Cys Thr Leu Gln Asp Pro Asp Gly Gln Arg  
85 90 95  
Asn Leu Ser Gly Lys Val Ile Leu Arg Val Thr  
100 105

<210> 98  
<211> 8  
<212> PRT  
<213> Oryctolagus cuniculus

<400> 98  
Gln Ser Val Tyr Asp Asn Asp Glu  
1 5

<210> 99  
<211> 720  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> A synthetic 96G08 anti-CD83 light chain sequence

<400> 99  
atggacacga gggccccac tcagctgctg gggctcctgc tgctctggct cccaggtgcc 60  
acatttgcg aagtgctgac ccagactgca tcgcccgtgt ctgcacctgt gggaggcaca 120  
gtcaccatca attgccagtc cagtcagagt gtttataata acgacttctt atcctgggat 180  
cagcagaaac cagggcagcc tcccaaactc ctgatctatt atgcatccac tctggcatct 240  
ggggtcccat cccggttcaa aggcagtgga tctgggacac agttcactct caccatcagc 300  
gacctggagt gtgacgatgc gccacttact actgtacagg cacttatggt aatagtgtt 360  
ggtacgagga tgctttcggc ggagggaccg aggtgggtgt caaacgtacg ccagttgcac 420  
ctactgtcct cctcttccca ccatctagcg ctgagctggc aactggaaca gccaccatcg 480  
tgtgcgtggc gaataaatac tttcccgatg gcaccgtcac ctggaagggt gatggcatca 540  
cccaaagcag cggcatcaat aacagtagaa caccgcagaa ttctgcagat tgtacctaca 600  
acctcagcag tactctgaca ctgagcagcg acgagtacaa cagccacgac gactacacct 660  
gccaggtggc ccaggactca ggctcaccgg tcgtccagag cttcagtagg aagagctgtt 720